

Genome Browser

Introduction

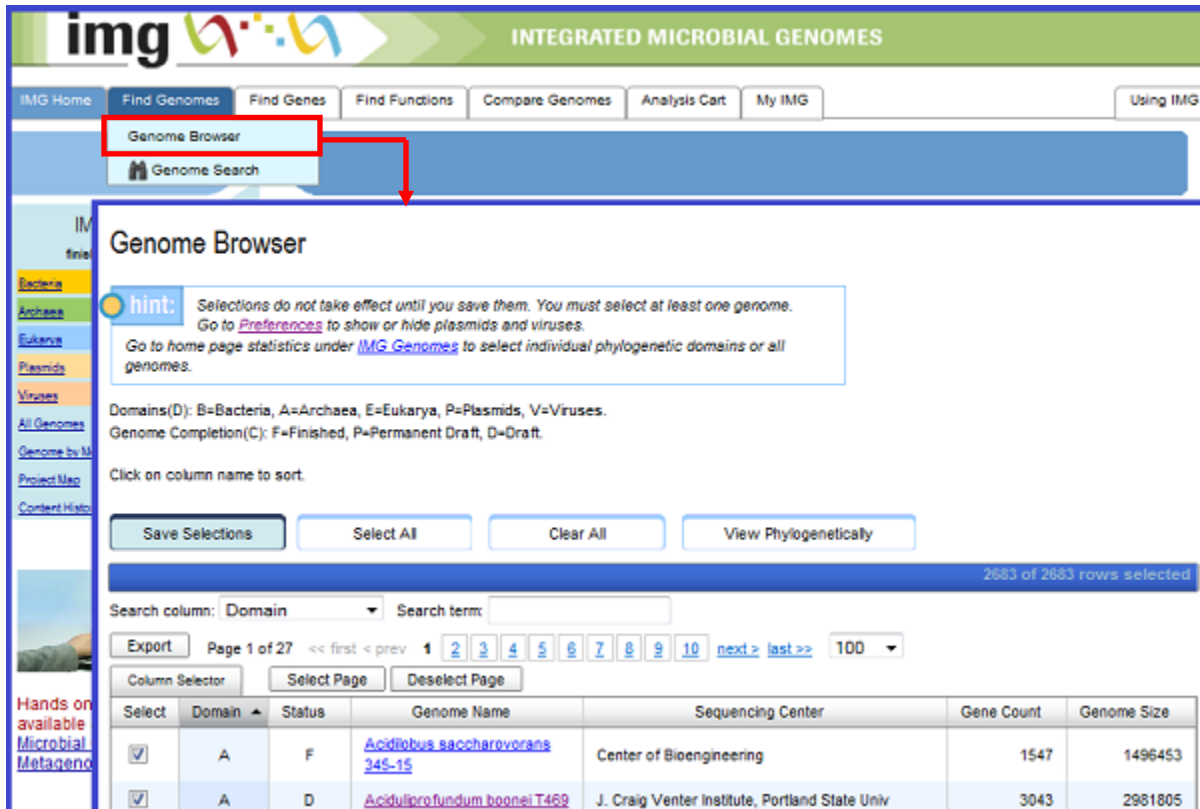
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Genome Browser

Genome Browser is a way for selecting and browsing genomes in IMG.

View Alphabetically

Genome Browser can be selected and viewed alphabetically via the second-level menu under **Find Genomes**, as shown in Figure 1.



The screenshot shows the IMG (Integrated Microbial Genomes) website. The top navigation bar includes links for IMG Home, Find Genomes, Find Genes, Find Functions, Compare Genomes, Analysis Cart, and My IMG. A red box highlights the 'Genome Browser' option under the 'Find Genomes' menu. The main content area is titled 'Genome Browser' and includes a hint box, instructions on domains and genome completion, and buttons for 'Save Selections', 'Select All', 'Clear All', and 'View Phylogenetically'. A table displays a list of genomes, with columns for Select, Domain, Status, Genome Name, Sequencing Center, Gene Count, and Genome Size. The table shows two genomes: *Acidithiobacillus ferrooxidans* and *Acidithiobacillus thiooxidans*.

Select	Domain	Status	Genome Name	Sequencing Center	Gene Count	Genome Size
<input checked="" type="checkbox"/>	A	F	Acidithiobacillus ferrooxidans 345-15	Center of Bioengineering	1547	1496453
<input checked="" type="checkbox"/>	A	D	Acidithiobacillus thiooxidans T469	J. Craig Venter Institute, Portland State Univ	3043	2981805

Figure 1: Genome Browser view alphabetically.

The **Genome Browser** allows user to select or de-select genomes individually or collectively. User can click on the name of an individual genome to view the associated **Organism Details**. User can also sort the alphabetical list of genomes by clicking on a column name. Alphabetical

columns are usually sorted in ascending order. Numeric columns are usually sorted in descending order (most to least significant).

User can *save* genomes selected with the **Genome Browser** by clicking the checkmark box next to each genome, and then clicking on "Save Selections" button. User also has the option to "Select All" of the genomes or "Clear All" of the selections.

The genomes user saved define the set of genomes for the IMG analysis tools such as **Gene Search**, **Gene Ortholog Neighborhoods**, **Phylogenetic Profiler**, **Genome Statistics**, and for highlighting in ortholog and homolog lists. These tools will be applied on this set of saved genomes, unless user *overrides* this selection via the provided **Genome Filter**. The box in the upper corner of the browser window displays how many genomes are selected for the current analysis tool.

Table Configuration

By default, the alphabetical list of genomes includes information on domain, completion status, sequencing center, gene count, genome size. However, user can configure the displayed columns by using the **Table Configuration** selector at the bottom of the **Gene Browser** page, as shown in Figure 2.

Table Configuration

Additional Output Columns

Expand All

Collapse All

Genome Field

☐ Taxon Object ID
☐ NCBI Taxon ID
☐ RefSeq Project ID
☐ GenBank Project ID
☐ Phylum
☐ Class
☐ Order
☐ Family
☐ Genus
☐ Species
☐ Strain
☒ Sequencing Center
☐ Funding Agency
☐ Add Date
☐ Is Public
☐ IMG Release
☐ IMG Product Assignment
☐ IMG Submission ID
☐ GOLD ID

Metadata Category

☐ Biotic Relationships
☐ Body Site
☐ Body Subsite
☐ Cell Arrangement
☐ Cell Shape
☐ Diseases
☐ Energy Source
☐ Ecosystem
☐ Ecosystem Category
☐ Ecosystem Type
☐ Ecosystem Subtype
☐ Specific Ecosystem
☐ Gram Staining
☐ Host Name
☐ Motility
☐ Metabolism
☐ Oxygen Requirement
☐ Phenotype
☐ Relevance
☐ Salinity
☐ Sporulation
☐ Temperature Range

Statistics Data

Display Genomes Again

Select All

Select Counts Only

Select Percentage Only

Clear All

Figure 2: Table Configuration selector.

The **Table Configuration** selector lists three groups of “Additional Output Columns”:

- Genome Field:
Taxon Object ID; NCBI Taxon ID; RefSeq Project ID; GenBank Project ID; Phylum; Class; Order; Family; Genus; Species; Strain; Sequencing Center; Funding Agency; Add Date; Is Public; IMG Release; IMG Product Assignment; IMG Submission ID; GOLD ID
- Metadata Category:
Biotic Relationships; Body Site; Body Subsite; Cell Arrangement; Cell Shape; Diseases; Energy Source; Ecosystem; Ecosystem Category; Ecosystem Type; Ecosystem Subtype; Specific Ecosystem; Gram Staining; Host Name; Motility; Metabolism; Oxygen Requirement; Phenotype; Relevance; Salinity; Sporulation; Temperature Range
- Statistics Data:
Scaffold Count; CRISPR Count; GC Count; GC %; Coding Base Count; Genome Size; Gene Count; CDS Count; CDS %; RNA Count; rRNA Count; 5S rRNA Count; 16S

rRNA Count; 18S rRNA Count; 23S rRNA Count; 28S rRNA Count; tRNA Count; Other RNA Count; Fused Count; Fused %; Fusion Component Count; Fusion component %; Pseudo Count; Pseudo %; Unchar Count; Unchar %; Obsolete Count; Obsolete %; Revised Count; Revised %; w/ Func Pred Count; w/ Func Pred %; w/o Func Pred Sim Count; w/o Func Pred Sim %; w/o Func Pred No Sim Count; w/o Func Pred No Sim %; Signal Peptide Count; Signal Peptide %; Transmembrane Count; Transmembrane %; SwissProt Count; SwissProt %; Not SwissProt Count; Not SwissProt %; SEED Count; SEED %; Not SEED Count; Not SEED %; COG Count; COG %; Pfam Count; Pfam %; TIGRfam Count; TIGRfam %; COG Cluster Count; Pfam Cluster Count; TIGRfam Cluster Count; InterPro Count; InterPro %; Enzyme Count; Enzyme %; TC Count; TC %; KEGG Count; KEGG %; Not KEGG Count; Not KEGG %; KO Count; KO %; Not KO Count; Not KO %; MetaCyc Count; MetaCyc %; Not MetaCyc Count; Not MetaCyc %; IMG Term Count; IMG Term %; IMG Pathway Count; IMG Pathway %; IMG Parts List Count; IMG Parts List %; Genome Property Count; Genome Property %; Chromosomal Cassette Gene Count; Chromosomal Cassette Gene %; Chromosomal Cassette Count

User can use “Expand All” and “Collapse All” buttons to show or hide the entire columns, or click on the top “+/-” symbols to display or hide columns in each group.

To select/deselect columns in **Table Configuration** selector, user simply needs to select/deselect the checkbox next to the column name. Or user can click on the checkbox next to the top group name, to select/deselect the whole group. There are provided “Select All”, “Select Counts Only”, “Select Percentage Only”, “Clear All” buttons at the bottom to facilitate such selections/de-selections.

To add/remove displayed columns in table, user first selects/deselects the column names in the **Table Configuration** selector, and then clicks the “Display Genomes Again” button to display.

View phylogenetically

The **Genome Browser** also permits user to select genomes from a list of genomes organized as a *phylogenetic tree*. The phylogenetical view can be accessed via the “View phylogenetically” button in the alphabetical list of genomes, or via the summaries on the **IMG home page**, as shown in Figure 3.

img INTEGRATED MICROBIAL GENOMES

IMG Home Find Genomes Find Genes Find Functions Compare Genomes Analysis Cart My IMG

IMG Genomes

	finished/draft/perm draft	Total
Bacteria	1159/1344/4	2507
Archaea	92/8/0	100
Eukarya	19/57/0	76
Plasmids	1155/1/0	1156
Viruses	2584/0/0	2584
All Genomes	5009/1410/4	6423

Genome by Metadata
Project Map
Content History

Hands on training available at the [Microbial Genomics & Metagenomics Workshop](#)

Genome Browser Archaea Tree

Save Selections View Alphabetically

Only visible selected genomes will be saved.
 ● Green dot to select
 ● Red dot to clear

Open All Close All

- 01 ▼ ● ● Archaea (100)
- 02 ▼ ● ● Crenarchaeota (29)
- 03 ▼ ● ● Thermoprotei (29)
- 04 ▼ ● ● Acidilobales (1)
- 04 ▼ ● ● Desulfurococcales (8)
- 04 ▼ ● ● Sulfolobales (12)
- 04 ▼ ● ● Thermoproteales (8)
- 05 ▼ ● ● Thermofilaceae (1)
- 05 ▼ ● ● Thermoproteaceae (7)
- 06 ▼ ● ● Caldivirga (1)
- 06 ▼ ● ● Pyrobaculum (4)
- 08 ☐ [Pyrobaculum aerophilum IM2](#) [F]
- 08 ☐ [Pyrobaculum arsenaticum DSM 13514](#) [F]
- 08 ☐ [Pyrobaculum caldifontis JCM 11548](#) [F]
- 08 ☐ [Pyrobaculum islandicum DSM 1484](#) [F]

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[Item Requirements](#)

[G](#) and [FAQ](#) on IMG.

Figure 3. Genome Brower view phylogenetically.

The genome summaries on the IMG home page provide links to subgroups of genomes that can be viewed in the **Genome Brower**. Click on an underlined value to load the list of genomes it represents. For example, user can quickly retrieve a list of all the archaeal genomes by clicking on Archaeal label in the summary table.

With the phylogenetic tree view, user can select or deselect all of the genomes in a particular taxonomic group.